



## Outbreak of Salmonella Choleraesuis in Danish pig herds

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# 6. Outbreak of *Salmonella* Choleraesuis in Danish pig herds

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In the end of 2012 one Danish pig herd was found positive for *Salmonella* Choleraesuis. This event was followed by the isolation of *S. Choleraesuis* from three herds during 2013 in January, August and December, respectively. In all herds there were signs of clinical disease. Finding *S. Choleraesuis* was unexpected since it is rarely found in pigs in Denmark and the last isolation was during an outbreak in 1999 [1]. Infections with *S. Choleraesuis* in humans are also very rare in Denmark. The last human case of *S. Choleraesuis* was in June 2012 and since 2000 only six cases has been reported.

At the National Food Institute, Technical University of Denmark, studies were initiated to investigate the possible connection between the infections. PFGE typing showed that the isolates from the three occasions (1999, 2012 and 2013) had different PFGE profiles, suggesting that several introductions of *S. Choleraesuis* to Denmark had occurred. Epidemiological investigations showed that pigs from the herd found positive in 2012 have been delivered to the herds found positive in January 2013, and that isolates from these two herds had the same PFGE profile. Isolates from the two herds infected in the second half of 2013 shared a different PFGE profile. It has not been possible to identify the primary introduction of the infection to the Danish pig herds. This was also the case for the outbreak in 1999/2000

[1]. Apart from the delivery of pigs from one farm to another taking place in December 2012 and January 2013, no new pigs had to our knowledge been brought into the infected herds, ruling out horizontal spread between herds as a source. Other plausible causes include cross contamination from contaminated vehicles during transport, contaminated feed, contact with infected humans and cross contamination from wildlife, but presently there is no clear evidence pointing at any of these sources.

The lack of source identification may have been caused by limitations in the epidemiological information available, but also by an insufficient resolution of isolates by the epidemiological typing methods applied (mainly PFGE and antimicrobial resistance profiles). Future use of methods with higher resolution, such as whole genome sequencing (see chapter 3 for more information), might help in revealing the source in this and other outbreaks.

## References

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